Agilent CytoGenomics 1.5

Running CytoGenomics Analyses

User Guide

Research Use Only. Not for Diagnostic Procedures

Agilent Technologies

Notices

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In This Guide...

This guide describes how to use the Agilent CytoGenomics 1.5 software to run workflows and display reports and aberrations. The functions described in this guide are typically performed by users with an assigned role of "Technician." However, tasks described in this guide are available to users with an assigned role of "Technician," "Scientist," or "Administrator."

1 Getting Started

This chapter gives an overview of the tasks required for running workflows to extract or import and analyze samples and display reports and aberrations.

2 Running and Monitoring Workflows

This chapter describes how to select and run manual and automated workflows. It also explains how to use the Job Monitor to find and check the status of workflow jobs.

3 Displaying Reports and Aberrations

This chapter describes how to display the reports and aberrations for completed workflows.

4 Reviewing and Signing Off Results

This chapter describes how to find and open analyzed samples, make changes, add notes, and sign off the results.

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1 Getting Started

In Agilent CytoGenomics 1.5, tasks in the Analysis tab let you run workflows that

- perform feature extraction
- analyze samples using selected filters and detection algorithms
- generate reports

After workflows are complete, you can

- display the results
- check in and out samples
- triage samples
- sign off samples (for users with role of Scientist or Administrator)

This chapter gives an overview of the tasks typically performed in the Analysis tab. The chapters that follow contain step-by-step instructions for performing those tasks.

For information on the tasks commonly performed by users with the Administrator role, see the *Installation and Administration Guide*. For information on setting up and quality review (typical tasks for the Scientist role), see the *Setup and Quality Review User Guide*. For information on windows, command ribbons, dialog boxes, and reports you see in the Agilent CytoGenomics 1.5 program, see the *Reference Guide*.

1 Getting Started

Overview of Tasks for Running Workflows and Displaying Results

The following diagram shows the main tasks performed when you run a workflow. Details on how to perform these tasks are given in the chapters that follow.

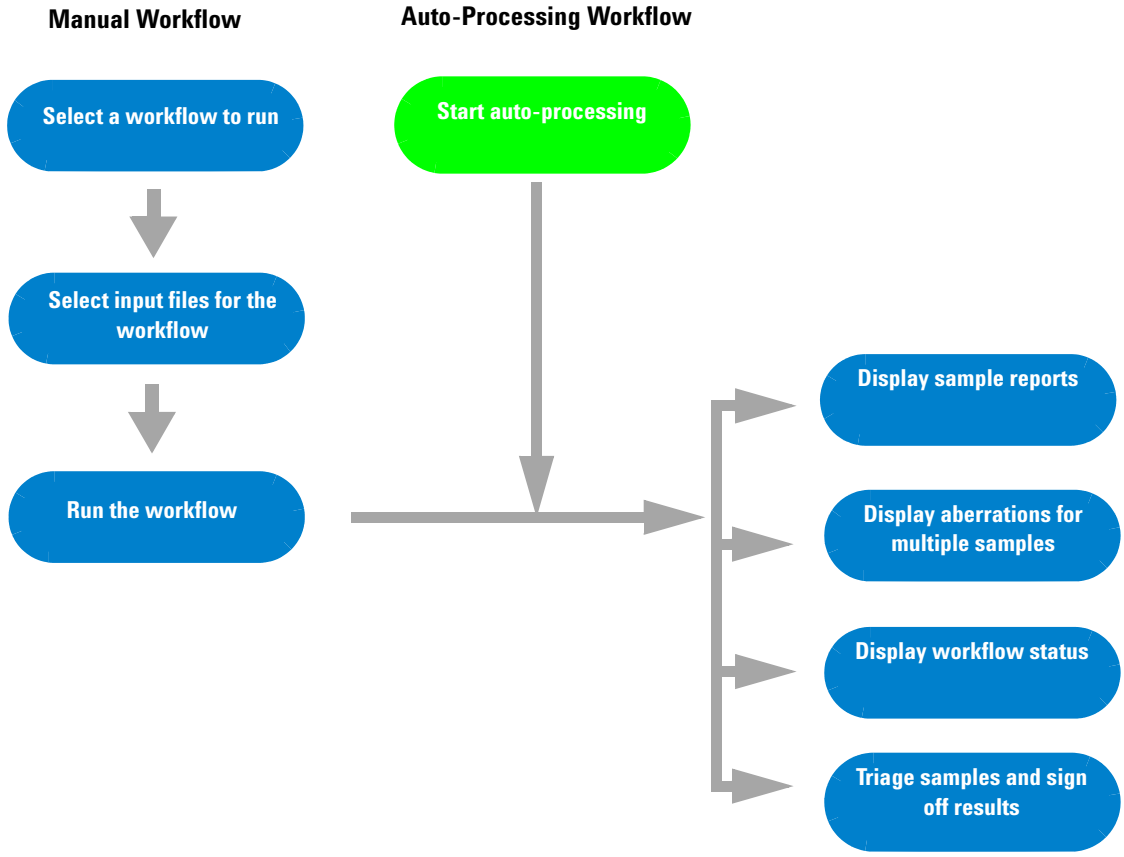

Figure 1 Typical CytoGenomics tasks for running workflows and displaying results

Getting Help

To get help within Agilent CytoGenomics 1.5

Agilent CytoGenomics 1.5 has several help guides. To open a help guide, on the right side of the Agilent CytoGenomics 1.5 tab ribbon, click the **Manuals** arrow. Then select the help guide you want to display. Help guides are opened in Adobe® Reader® software.

Help videos are also available from within the Agilent CytoGenomics 1.5 program. These short videos provide brief instructions for doing basic tasks within Agilent CytoGenomics 1.5. To start a help video, on the right side of the Agilent CytoGenomics 1.5 tab ribbon, click **Help Videos**. Then select the video you want to watch.

To contact Agilent Technical Support

Technical support is available by phone and/or e-mail message. A variety of useful information is also available on the Agilent Technical Support Web site.

Resource	To find technical support contact information
Agilent Technical Support Web site	**1** Go to http://chem.agilent.com. **2** Select a country or area. **3** Under Quick Links, select **Technical Support**. **4** Select from the available links to display support information.
Contact Agilent Technical Support by telephone or e-mail message (United States and Canada)	Telephone: (800-227-9770) E-mail message: informatics_support@agilent.com
Contact Agilent Technical Support by telephone or e-mail message (for your country)	**1** Go to http://chem.agilent.com. **2** Select **Contact Us**. **3** Under Worldwide Sales and Support Phone Assistance, click to select a country, and then click **Go**. Complete e-mail message and telephone contact information for your country is displayed.

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1 Getting Started

To learn about Agilent products and services

2 Running and Monitoring Workflows

In Agilent CytoGenomics 1.5, *workflows* are used to automate feature extraction and/or analysis of CGH and CGH+SNP microarrays. Each workflow contains a set of actions and parameters for analyzing and reporting the data during the workflow. Workflows are set up by users in your laboratory with the role of Scientist or Administrator. Once the workflows are configured and published, users with any role can run them.

When you run a workflow in *manual* mode, you start the workflow and select the input files. When you run a workflow in *auto-processing* mode, the workflow automatically picks up and uses image files as they are placed in a designated folder by a scanner. This chapter describes how to select and run a workflow in manual or auto-processing mode, and how to search for and display the status of workflows.

Running Workflows Manually

This section describes how to select and run a workflow in manual mode. A manual workflow extracts and/or analyzes one or many samples that you select when you start the workflow. Each time a workflow is started, it is assigned a Job Name and Description, which is used to track and monitor the status of the workflow, as described later in this chapter.

The following diagram shows the steps for running a manual workflow.

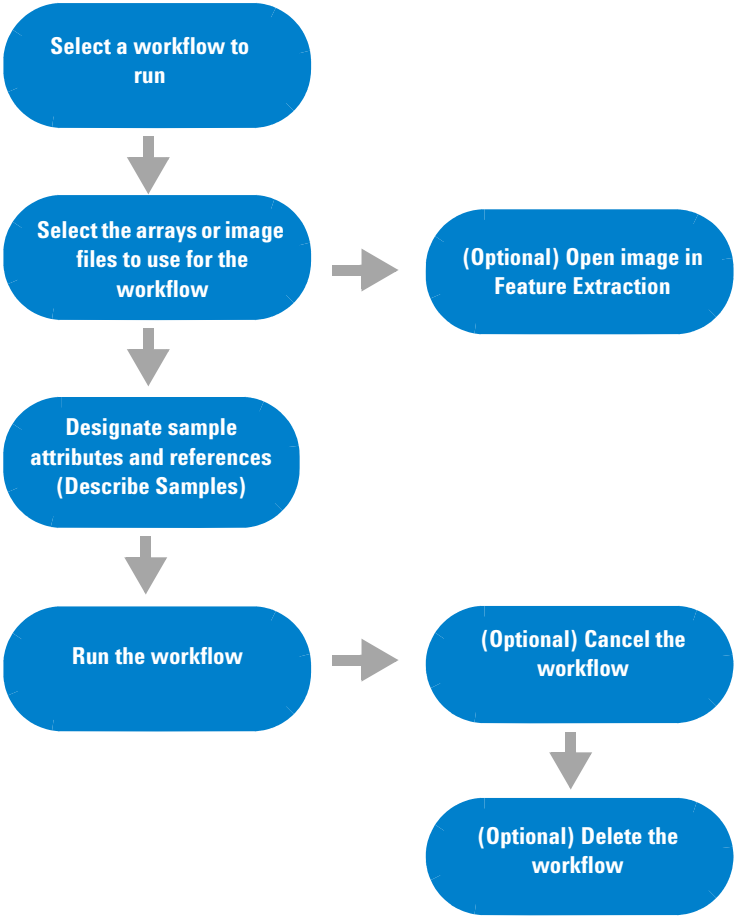

Figure 2 Tasks for running a manual workflow

Table 1 Tasks for running a manual workflow

To do this task	Follow these instructions	Comments
Select a workflow to run	**1** In the Analysis tab, click **Analyze**  . **2** Under Select Workflow, select the workflow from the list. The program creates a job name and description, based on the workflow name, date, and time. **3** (Optional) Under Job Name, type a job name to use for the workflow run, if you do not want to use the default job name. **4** (Optional) Under Description, type a description for the workflow run. **5** Select the files to use for workflow input. The type of files required for the workflow are determined by the selected workflow. See the following sections for a description of how to select input files for a workflow.	• By default, the job name is the workflow name followed by the date and time. • You can run published workflows that were created by users with the role of "Scientist" or "Administrator." • If you have the role of "Scientist" or "Administrator", you can run a private workflow that you created. • The input for a workflow can be image files (for feature extraction + analysis workflows), extracted feature extraction files, or files that were already imported. The workflow you select determines what kind of files you must select. • To make the selected workflow the default workflow for running jobs, select **Set it as default workflow for running the Job**.

Table 1 Tasks for running a manual workflow (continued)

To do this task	Follow these instructions	Comments
Select image files for the workflow (for workflows that extract images)	**1** Select a workflow to run. See Select a workflow to run. **2** At the bottom of the Import Image Files pane, click **Add TIFF Image(s)**. The Open dialog box appears. By default, the folder displayed is the default image file folder that was set up by the Scientist. **3** If necessary, browse to the folder where the microarray image (.tif) file is located. **4** Select the image file, and click **Open**. The Add image pack information for FE Extraction dialog box appears. **5** Click **Add Images**. The images appear in the Import Image Files table. **6** (Optional) For each image, double-click Image Note, and type information about the image. **7** Click **Next** to describe samples and start the workflow.	• If you select a workflow that is designed to do feature extraction before the analysis, you must select image files for the workflow input. • For information on the Import Image Files pane, see the *Reference Guide*. • If no design exists in the database for an image you select, you must go to the Content tab and import the image file first. Otherwise, you will not be able to run the workflow. Only users with the role of "Scientist" or "Administrator" can import a design.
Select extracted FE files for the workflow (for workflows that analyze extracted images)	**1** Select a workflow to run. See Select a workflow to run. **2** In the Import FE Files pane, click **Add Arrays**. The Open dialog box appears. By default, the folder displayed is the default image file folder that was set up by the Scientist or Administrator. **3** If necessary, browse to the folder where the feature extracted file (.txt) is located. **4** Select the file to import, and click **Open**. The selected file appears in the Import FE Files table. **5** Click **Next** to Describe Samples and start the workflow.	• If you select a workflow that imports extracted Feature Extraction (FE) files before analysis, you must select the extracted files for the workflow input. • In order to import an FE file in a workflow, the design that matches the file must be present in the database.

Table 1 Tasks for running a manual workflow (continued)

To do this task	Follow these instructions	Comments
Select imported data for the workflow (rerun analysis)	**1** Select a workflow to run. See Select a workflow to run. **2** In the Select Imported Data pane, under Select Design, select the design for the imported data. **3** Under Select Genome Build, click to select the build for the design. The available arrays for the selected design and build appear in the Array List. **4** Select the array(s) you wish to analyze with the workflow. Use the > and >> buttons to move one or all of the arrays to the Selected Array List. Use the < and << buttons to remove one or all of the arrays from the Selected Array List. **5** Click **Next** to Describe Samples and start the workflow.	• To rerun an analysis, use a workflow that uses data that is already in the database (imported data).
(Optional) Add a design to the database	**1** Select a workflow to run that requires extracted FE files. See Select a workflow to run. **2** Select one or more extracted FE files to import. See Select extracted FE files for the workflow (for workflows that analyze extracted images). If you selected a file without a matching design in the database, the Design Status will show **Not Found**. In addition, the Add Designs button will be active. **3** At the bottom of the workflow table, click **Add Designs**. The Open dialog box appears. **4** Search for the location for the design, click to select it, and then click **Open**. The Design Status for the sample changes to **Path Provided.**	• The Add Designs function is only available for workflows that import already-extracted FE files.

Table 1 Tasks for running a manual workflow (continued)

To do this task	Follow these instructions	Comments
(Optional) Open an image in Feature Extraction	**1** Select a workflow to run that extracts images. See Select a workflow to run. **2** Add one or more Tiff images to the workflow. **3** In the Import Image Files table, under **View Image in FE**, click **View Image**. The Feature Extraction for Cyto program opens with the selected image displayed.	• For information how to zoom the image and change the display options, see the *Feature Extraction for Cyto User Guide*. You can open this guide from the Help menu in the Feature Extraction for Cyto program.
Describe Samples	**1** After you select the input files for a workflow, at the bottom of the workflow window, click **Next**. The Describe Samples pane appears. **2** To show or hide attributes for the sample, click **Show/Hide Attributes**. The Show/Hide Attributes dialog box appears where you mark or clear the attributes to display. **3** To select or change an attribute for a sample, select or change it in the column for the selected array. **4** For CGH+SNP arrays, select a genotype reference, if one is not already selected. **5** Click **Save Changes**. **6** To go back to the workflow window, click **<<Back**. **7** To run the workflow, click **Run**.	• The Describe Samples pane shows the samples for the current workflow. You can show or hide attributes for the samples in the workflow, and select or change the attributes. • To go back to the workflow window, use the <<Back button. Otherwise, you will lose the selected samples for the workflow. • For CGH+SNP analysis, each array must have a genotype reference selected for the Green Sample attribute. (Use Red Sample for dye-flipped arrays.) • Once a file is imported or analyzed, you can no longer change the *required* sample attributes. (Array ID, Global Display Name, Green Sample, Red Sample, and Polarity)

Table 1 Tasks for running a manual workflow (continued)

To do this task	Follow these instructions	Comments
Run the workflow	**1** Select a workflow to run. See Select a workflow to run. **2** Select one or more images or files for the workflow input, and then click **Next**. **3** Specify sample attributes, as required. See Describe Samples. **4** At the bottom of the Analysis Describe Samples window, click **Run**. The job monitor window appears, with the workflow and its status at the top of the workflow list.	• In order to see the Describe Samples window and run the workflow, you first select the required input file(s) for the selected workflow, and then click **Next**. • On 32-bit machines, if you start a workflow while another workflow is running, the second workflow waits until the first is complete before it runs.
(Optional) Cancel the workflow	**1** In the Analysis tab, click **Monitor**.  The workflow job monitor table appears. **2** In the job monitor table, in the row for the workflow you want to cancel, click **Cancel**.	• Once a workflow has completed or failed, the Cancel button is no longer available.
(Optional) Delete a workflow	**1** In the Analysis tab, click **Monitor**.  The workflow job monitor table appears. **2** In the job monitor table, in the row for the workflow you want to delete, click **Delete**.	• You cannot delete a running workflow. You must first cancel the workflow and then delete it. • You cannot delete a completed workflow.

Running Auto-Processing Workflows

Auto-processing workflows automatically extract and analyze scanned image files as they are deposited by an Agilent scanner into a designated folder. Before running an auto-processing workflow, the workflow must be configured by a user with the role of "Scientist" or "Administrator." For information on how to configure auto-processing workflows, see the *Setup and Quality Review User Guide*. This section describes how to start a workflow in auto-processing mode.

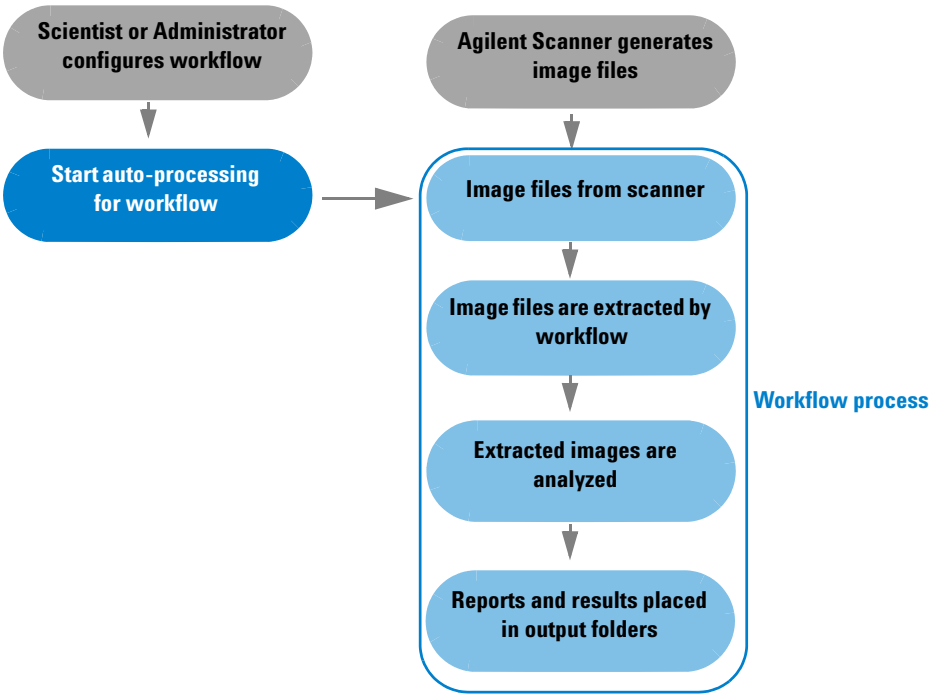

Figure 3 Overview of auto-processing workflows

The following table describes the tasks required for running an auto-processing workflow.

Table 2 Tasks for running an auto-processing workflow

To do this task	Follow these instructions	Comments

Start auto-processing for workflow	• In the Analysis tab, under Auto-Processing, click the start button. 	• Images placed in the auto-processing workflow Tiff image input directory are processed automatically. They are analyzed using the default workflow selected in the Auto-Processing Settings for the image design. These settings are configured by a user with the role of Scientist or Administrator.
		• In order to run an auto-processing workflow, sample information must be available either:
		  ◦ in the Content tab
		  ◦ in one or more sample information files (SAF) in the configured SAF File Input Directory
		• SAF files, if present in the SAF File Input Directory, are automatically imported by the auto-processing workflow.
		• Auto-processing workflow jobs appear in the Job Monitor window, with Type *Automated*.
		• The auto-processing workflow continues until the user stops the auto-processing.

Table 2 Tasks for running an auto-processing workflow (continued)

To do this task	Follow these instructions	Comments
Stop auto-processing for workflow	• In the Analysis tab, under Auto-Processing, click the stop button. 	• When you stop an auto-processing workflow, the sample currently in process will complete before the workflow is stopped.
View Auto-Processing Logs	**1** In the Analysis tab, under Auto-Processing, click **Logs**. A list of auto-processing workflows appears. **2** In a workflow row, under Action, click **View**. The auto-processing log for that workflow appears. **3** Click **Refresh** to update the information in the log.	• When you stop auto-processing, the list of auto-processing logs is cleared.

Searching for Jobs

When a workflow is started, it is added to the jobs list in the Analysis Job Monitor window. This window is a convenient way to see the status of all jobs, and to find and display the results from completed workflow jobs.

Table 3 describes how you use the Job Monitor to search for and manage workflow jobs.

Table 3 Tasks for searching for and displaying workflow jobs

To do this task	Follow these instructions	Comments
Search for a job	**1** In the Analysis tab, click **Monitor**.  The workflow job monitor table appears. **2** Next to Search Type, click the arrow and select the parameter to use to search for workflow jobs. **3** Next to Value, click the arrow, and select the value to match for the job search. OR Type the value to match for the job search. **4** Click **Search**. The jobs that match the selected criterion are displayed in the table.	• Click the **Reset** button to reset the table to display all jobs.
Delete a job	**1** In the Analysis tab, click **Monitor**.  The workflow job monitor table appears. **2** In the row for the job you want to delete, under Actions, click **Delete**.	• You cannot delete a job whose Status is **Running**, or **Waiting.** To delete a running job, you must Cancel it first.

Table 3 Tasks for searching for and displaying workflow jobs (continued)

To do this task	Follow these instructions	Comments
Display the job summary	**1** In the Analysis tab, click **Monitor**.  The workflow job monitor table appears. **2** In the job row, under Actions, click **View**. The Job Summary is displayed. **3** (Optional) Click **Save Log File**. The Save Log file dialog box opens. **a** Browse to a location where you want to save the log file. **b** In File name, type the name for the log file. **c** Click **Save**. **4** To close the Job Summary, click **Close**.	
Open a report from the job summary	**1** In the Analysis tab, click **Monitor**.  The workflow job monitor table appears. **2** In the job row, under Actions, click **View**. The Job Summary is displayed. Links to generated reports are displayed in blue. **3** Click the link for the report you want to display. The report PDF is displayed.	• Reports are opened from the workflow data output folders that were configured by users with a role of Scientist or Administrator.

Sending Results to Cartagenia BENCH

You can send analyzed samples to send to Cartagenia BENCH, if you have a valid Cartagenia BENCH account. Samples are sent to Cartagenia BENCH automatically as part of the workflow, or are sent manually using Analysis > Partners > Cartagenia BENCH.

The following are required in order to send results to Cartagenia BENCH:

- The Agilent CytoGenomics program must be configured in Config > Partners to send data to Cartagenia BENCH with a valid user name and password.
- The Agilent CytoGenomics program must be configured in Config > Partners to send one or more reports to Cartagenia BENCH.
- (For automated transfer of data to Cartagenia BENCH) The workflow must be configured to send data to Cartagenia BENCH.
- The workflow must generate the same reports as those selected in Config > Partners for Cartagenia BENCH.
- The design build for the data must be supported by Cartagenia.

In order to configure Agilent CytoGenomics for Cartagenia data transfer, you must have a user role of Scientist or Administrator. For information on how to configure Cartagenia BENCH, see the *Setup and Quality Review User Guide*.

Table 4 Tasks for sending data to Cartagenia BENCH

To do this task	Follow these instructions	Comments
Send data to Cartagenia BENCH as part of a workflow	**1** Configure the workflow to send data to Cartagenia BENCH. (For details, see the *Setup and Quality Review User Guide*.) **2** Make sure the workflow is configured to generate the same reports as those in Config > Partners for Cartagenia BENCH. **3** Make sure the data is of a design build that is supported by Cartagenia BENCH (for example, hg(18)). **4** Start the workflow run, either manually or with auto-processing.	• In order to configure workflows and Cartagenia BENCH data transfer, your user role must be Administrator or Scientist. • Users with any role can start a workflow in manual or auto-processing mode.

Table 4 Tasks for sending data to Cartagenia BENCH (continued)

To do this task	Follow these instructions	Comments
Search for samples to send to Cartagenia	**1** In the Analysis tab, click **Partners**. The Cartagenia BENCH tab appears. **2** Under Search Criteria**,** next to **Search**, select **Sent Status, Sign-off Date,** or **Attributes**. **3** For Sent Status**,** **a** Next to **Operator**, select a logical operator to apply to the value. **b** Next to **Value**, select the upload status to which the operator is applied for the search. OR For Sign-off Date, **a** Next to **Operator**, select a logical operator to apply to the date. **b** Next to **Value**, select the date to which the operator is applied for the search. OR For Attributes, **a** Next to **Attribute Name**, click the arrow and select a sample attribute to use for the search. **a** Next to **Operator**. select a logical operator to apply to the selected attribute. **b** Next to **Value**, click the arrow and select an attribute value to which the operator is applied for the search. **4** Click **Search**. The samples that match the search criteria are displayed in the table.	• Click **Reset** to set the search parameters to the default settings. • To remove the results of a search from the table, click **Clear Results**.

Table 4 Tasks for sending data to Cartagenia BENCH (continued)

To do this task	Follow these instructions	Comments
Send sample results to Cartagenia BENCH manually	**1** Search for the samples you want to send to Cartagenia BENCH, as described in Search for samples to send to Cartagenia BENCH, above. **2** In the sample list, under **Select**, select the samples you wish to send to Cartagenia BENCH. **3** Click **Send Now**. The Upload Status dialog box appears that shows the status of the upload task. **4** For workflows that failed, the reason for the failure is displayed.	• To send a single sample, click **Send Now** in its Upload Status. • Although the results of a search include all samples that match the criteria, only samples that generated the configured reports for Cartagenia BENCH are sent. • If an error occurs, the Upload Status shows "Error". Click **Error** to show the Cartagenia BENCH Log Record Status Error dialog box with details of the error.
Search for samples sent successfully or with errors	**1** In the Analysis tab, click **Partners**. The Cartagenia BENCH tab appears. **2** Under Search Criteria**,** next to **Search**, click the arrow and select **Sent Status**. **3** Next to Operator, the only option for Sent Status is "=". **4** Next to **Value**, click the arrow and select **Sent Successfully**, or **Error**. A list of the samples that were sent successfully or those that were not sent and generated errors are displayed.	

3 Displaying Reports and Aberrations

This chapter gives instructions on how to display reports and aberration results after workflow analyses are completed.

Searching for Analyzed Samples

In order to display reports or analysis results, you must first search for the samples you want to show. You set up and search for samples at the top of the window that appears when you click **Report** or **Multi Sample** on the Analysis command ribbon. The following diagram gives an overview of how to search for analyzed samples in the Report or View Multi Sample windows.

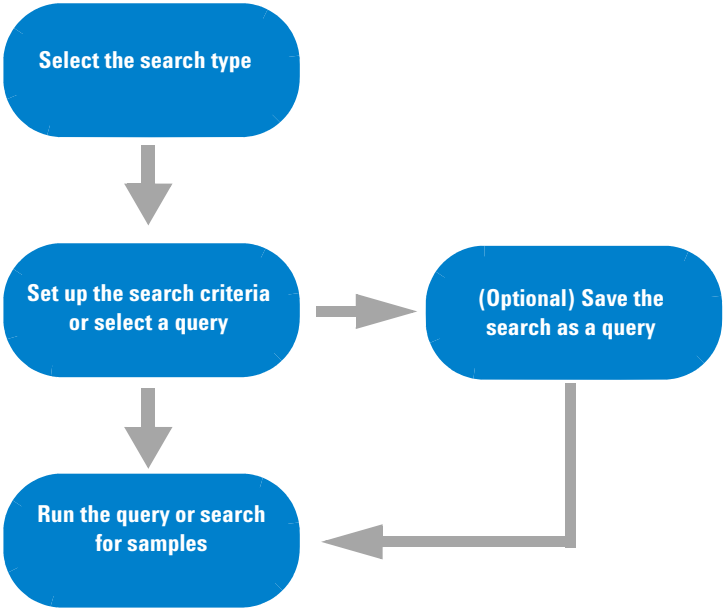

Figure 4 Searching for workflows

The following table gives instructions on how to set up searches and queries for finding analyzed samples.

Table 5 Tasks for setting up queries and searching for samples

To do this task	Follow these instructions	Comments
Set up a simple search	**1** In the Analysis command ribbon, click **Report**  or click **Multi Sample**  . **2** Next to **Search Type**, select **Simple Search**. **3** Next to **String Search**, type a string of text or characters to search for. **4** Click **Run**. The samples that contain the string are displayed in the table.	• To clear the results of your search, click **Clear Results** at the bottom of the window. • By default, the program displays the last 10 samples with cyto reports or analyzed results.
Set up and run an Advanced Search	**1** In the Analysis command ribbon, click **Report**  or click **Multi Sample**  . **2** Next to **Search Type**, select **Advanced Search**. **3** Under **Sample Attribute**, click the arrow and select one of the available attributes to use for the search. **4** Select **Is in range** or **Matches Value**. **5** If you select **Is in range**, under **Range**, type a start and stop value. The program searches for any value of the attribute that falls within that range. OR If you select **Matches Value**, under **Attribute Value**, type the value or text you want to match to the sample attribute, or (depending on the selected attribute) select a value from the list presented. **6** Click **Add**. The criterion is added to the Conditions for the query.	• **Is in range** or **Matches Value** are available depending on the sample attribute you select for an Advanced Search. • Logical Operation of **AND** will match samples only if both conditions are true. Logical Operation of **OR** will match samples if any of the conditions are true. • To remove all conditions for a query and start again, click **Clear Conditions**. • To clear the results of your search, click **Clear Results** at the bottom of the window.

Table 5 Tasks for setting up queries and searching for samples (continued)

To do this task	Follow these instructions	Comments
	7 (Optional) Under Logical Operation, click the arrow and select the logic to apply for the next condition. • Perform step 3 through step 6 until all conditions are set up. **8** Click **Execute** to run the search. Samples that match the search appear in the table.	
Save a search query	**1** Set up a search query. See Set up and run an Advanced Search, above. **2** Click **Save Query** to save the query conditions. The Input dialog box appears. **3** Type a name for the query. **4** Click **OK**.	
Run a saved search query	**1** In the Analysis command ribbon, click **Report**  or click **Multi Sample**  . **2** Next to **Search Type**, click the arrow and select **Query Search**. **3** Next to **Select Query,** click the arrow and select the query you want to run. **4** Under the conditions table, click **Execute**. The program runs the query and displays a list of the samples that meet the query conditions.	• A default query, "Last 10 records," displays the 10 most recent workflows. • Custom queries are created in the Config tab. You can also save the conditions you set up as an Advanced Search as a query. See Save a search query. • To clear the results of your search, click **Clear Results** at the bottom of the window.

Displaying Cyto Reports

After a workflow is completed, you can search for a sample and display the cyto report that was created for that sample. The diagram below shows the steps you use to search for a sample and display its cyto report.

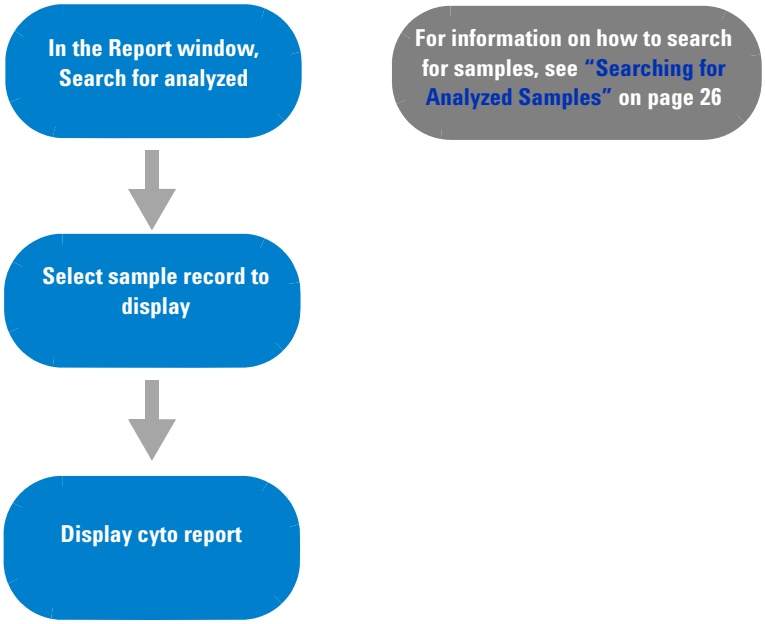

Figure 5 Displaying cyto reports

The table below shows how to display cyto reports for analyzed workflow samples.

To display cyto reports

The tasks in this section show you how to display cyto reports for samples in a completed workflow.

Table 6 Tasks for displaying reports

To do this task	Follow these instructions	Comments
Display cyto report for selected sample	**1** In the Analysis tab, click **Report.** **2** Search for samples. See "Searching for Analyzed Samples" on page 26, above. The search returns only samples for which a cyto report exists. **3** In the Table View, under Select, mark the workflow sample for which you want to display the cyto report. OR In Genomic View, under Select, mark the box next to the sample depicted in the genomic view of the samples. **4** At the bottom of the window, click **View Report**. The View Report dialog box appears. **5** Under Select Report, click the arrow, and select the report you want to display (if more than one cyto report exists for the sample). **6** Click **OK**. The Manage Cyto Report dialog box appears with the selected report displayed.	• Triage reports (sign off reports) are available only for samples that were signed off and have a Status of **Reviewed**. • From within the Manage Cyto Report dialog box, you can move through report pages, make changes to editable text fields, export, or print the report. For more information, see the *Reference Guide*.

Displaying Aberrations

After a workflow is completed, you can search for samples and display the aberrations in the View Aberrations window. In the View Aberrations window, extracted data and analysis results are tabulated and displayed next to depictions of the genome, selected chromosome, and selected genes of the species whose array data you are analyzing. Unlike the Triage View, in the View Aberrations window you can open more than one sample and display aberrations overlaid or side-by-side for comparison. In addition, you can create differential aberration, graphical penetrance, or graphical interval penetrance summaries. For more information about the View Aberrations window and its features, see the *Reference Guide*.

The following flowchart shows the steps you use to search for analyzed samples and display the results in the View Aberrations window.

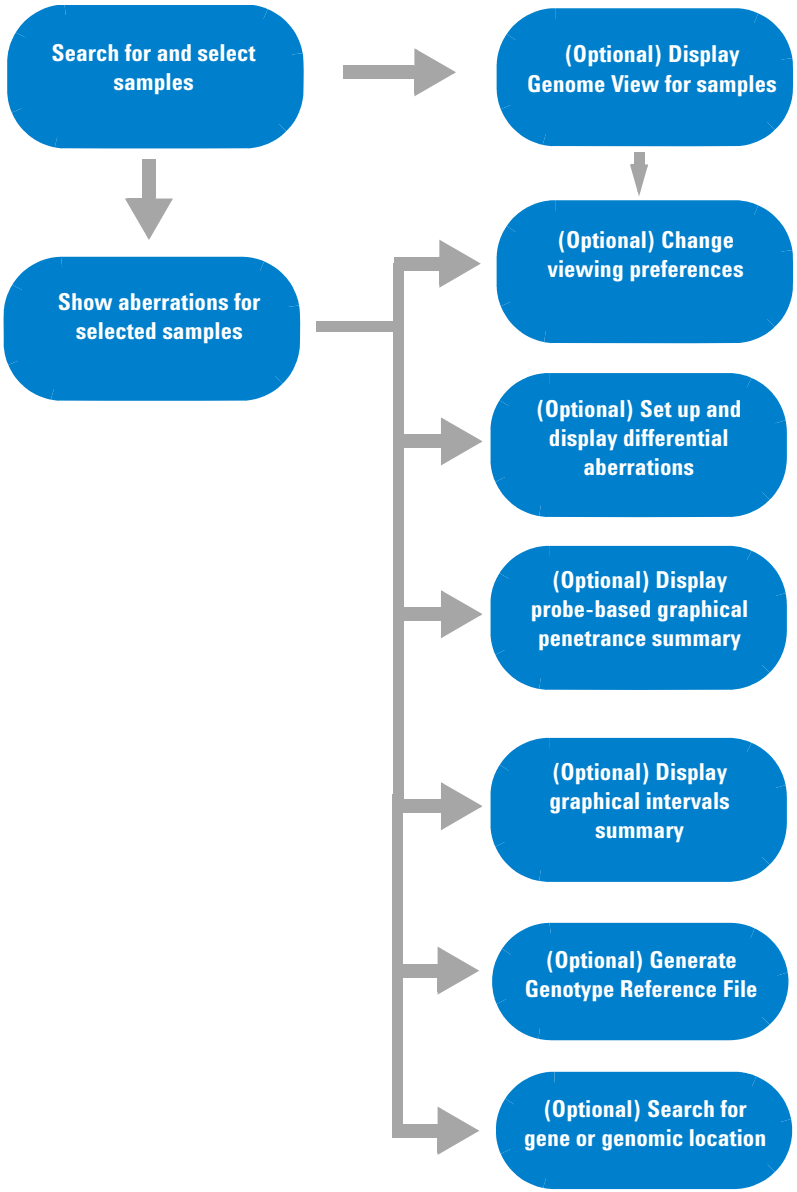

Figure 6 Displaying aberrations for analyzed samples

To display aberrations

The following table gives instructions on how to display aberrations within the View Aberrations window.

Table 7 Tasks for displaying aberration results

To do this task	Follow these instructions	Comments
Search for samples	**1** In the command ribbon of the Analysis tab, click **Multi Sample**  . **2** Search for the sample(s) of interest. For instructions, see "Searching for Analyzed Samples" on page 26. A list of samples that match the search conditions appear in the Table View.	
(Optional) Display Genome View for samples	**1** In the command ribbon of the Analysis tab, click **Multi Sample**  . **2** Search for samples to display. For instructions, see "Searching for Analyzed Samples" on page 26. A list of samples that match the search conditions appear in the Table View. **3** Click the **Genomic View** tab. A graphical display of all samples that meet the search conditions appears.	

Table 7 Tasks for displaying aberration results (continued)

To do this task	Follow these instructions	Comments
Show aberrations for selected samples	**1** In the command ribbon of the Analysis tab, click **Multi Sample**  . **2** Search for the sample(s) of interest. For instructions, see "Searching for Analyzed Samples" on page 26. A list of samples that match the search conditions appear in the Table View. **3** In the Table View or Genomic View, under **Select**, mark the workflow samples for which you want to display aberrations. **4** At the bottom of the Analysis window, click **View Aberrations**. The View Aberrations window appears with the results for the selected samples.	• For information on the items displayed in the View Aberrations window, and the View Preferences options, see the *Reference Guide*.
(Optional) Change viewing preferences	**1** Open one or more samples in the View Aberrations window. See Show aberrations for selected samples, above. **2** In the View Aberrations window, click **Settings**  . The View Preferences dialog box appears. **3** In the View Preferences dialog box, select the items you want to display, and select other viewing preferences.	• For information on the items displayed in the View Aberrations window, and the View Preferences options, see the *Reference Guide*.

Table 7 Tasks for displaying aberration results (continued)

To do this task	Follow these instructions	Comments
(Optional) Generate Genotype Reference File	**1** Open one or more samples in the View Aberrations window. See Show aberrations for selected samples, above. **2** In the command ribbon, click SNP.  The Generating Genotype Reference File dialog box is displayed. **3** In the Generating Genotype Reference Files dialog box, select the sample(s) to include in the genotype reference file. **4** Under Input Parameters, type a Confidence Threshold. **5** Under Input Parameters, select a Level of confidence. **6** Click **Browse** and select a location to save the new genotype reference file. **7** Click **OK** to generate the new genotype reference file. The file is saved in the specified location, with the name GenotypeReference_<Date>_<Design>_<Build>.txt.	• If you have a reference sample that is not genotyped, this creates a genotype reference for that sample using the Agilent-provided or known genotype references available in the database. The genotype calls generated using the known genotype reference are used, along with a user-supplied confidence threshold and level, to generate a genotype reference file. This "custom" genotype reference file can then be imported to the database, and used to analyze additional CGH+SNP microarrays. • In order to generate a genotype reference file, the Red Sample field for each microarray (Green for dye-flipped,) must contain the unknown reference sample name. A validated genotype reference must be selected in the other sample channel.

Table 7 Tasks for displaying aberration results (continued)

To do this task	Follow these instructions	Comments
(Optional) Create a custom track	**1** Open an analyzed sample in Triage View or the View Aberrations window. See Show aberrations for selected samples, above. **2** Right- click anywhere within the log ratio plot area in Gene View, then click **Create Track**. The Create Track dialog box appears. See "Create Track" on page 304. **3** In the dialog box, set the Name, Description and Color. **4** In the dialog box, **a** Select **User Defined**. **b** Under **Chromosome**, select the chromosome for the track. **c** Under **Start** and **Stop**, type the start and stop of the region for the new track. **d** Under **Select Track Source**, click **Aberration Results**. OR, to generate a track for the entire gene **a** Select **For complete gene view**. **b** Under **Select Track Source**, click **Aberration Results**. OR, to generate a track for current the region defined by the cursor **a** Select **For aberrant region below cursor**. **b** Under **Chromosome**, select the chromosome for the track. **c** Under **Start** and **Stop**, type the start and stop of the region for the new track. **d** Under **Select Track Source**, click **Aberration Results**. **5** Click **OK**.	• When you create a track, you create a list of the genes in a contiguous chromosomal region that you select. • You can turn on and off the display of tracks in the Gene View and in Reports from the Track Settings dialog box. See the *Reference Guide* for information on the Track Settings dialog box. • You can also create a custom track from a query in Config > Tracks > Create Track From Query. For more information, see the *Setup and Quality Review User Guide*.

Table 7 Tasks for displaying aberration results (continued)

To do this task	Follow these instructions	Comments
(Optional) Create a signal intensity bar chart	**1** Open an analyzed sample in Triage View or the View Aberrations window. See Show aberrations for selected samples, above. **2** Right- click anywhere within the log ratio plot area in Gene View, then click **Show Intensity Bar Charts**. The Create Signal Bar Chart dialog box appears. **3** Under Set Chromosome Start-Stop, select the region to use for creating the bar chart. Choices include a user-defined region, the complete gene view, or for the current region selected by the cursor. **4** Click **OK**. A Median Signal Intensity bar chart is created showing red and green signal intensities for all selected microarrays.	• A signal bar chart is a histogram that displays the median signal intensities in a genomic region of selected Agilent arrays. • If you have more than one sample open in the View Aberrations window, a bar chart is created for all selected arrays. • For more information on the Create Signal Bar Chart dialog box, see the *Reference Guide*.
(Optional) Display track in UCSC browser	**1** Open an analyzed sample in Triage View or the View Aberrations window. See Show aberrations for selected samples, above. **2** Right-click Gene View, and click **Show in UCSC**. The View coordinates in UCSC browser dialog box appears. **3** Complete the dialog box with the track parameters, and click **OK**. The UCSC Browser appears, if you are connected to the Internet. You may need to enable pop-ups or set other preferences on the UCSC Web site; see the browser help for information.	• For information on opening analyzed samples in Triage View, see"Tasks for Reviewing and Signing Off Results" on page 48. • For more information on the View Aberrations window, see the *Reference Guide.*

Table 7 Tasks for displaying aberration results (continued)

To do this task	Follow these instructions	Comments
(Optional) Change how tracks are displayed	**1** Open an analyzed sample in Triage View or the View Aberrations window. See Show aberrations for selected samples, above. **2** Right-click anywhere within the log ratio plot area in Gene View, and click **Track Settings**. The Track Settings dialog box appears. **3** Select tracks and how to display them. **4** Click **OK**.	• For more information on the Track Settings dialog box, see the *Reference Guide*.
(Optional) Search for gene or genomic location	**1** Open an analyzed sample in Triage View or the View Aberrations window. See Show aberrations for selected samples, above. **2** On the command ribbon, click **Go to**. The Go to Gene/Genomic location dialog box appears. **3** Under RefSeq by Symbol, select a gene to search for. OR Under Genomic Location, select a chromosome and then type a base position to search for. **4** Click **Go**. The program finds the gene or genomic location in the Genomic Viewer.	• It can take several seconds or more to display the Go to Gene/Genomic location dialog box. This is because the program searches for all the genes in the sample.

To display aberration summaries

From within the View Aberrations window, you can set up and display a variety of aberration summaries. These summaries are helpful in comparing and evaluating aberration results from a series of samples.

Table 8 Tasks for creating aberration summaries

To do this task	Follow these instructions	Comments
(Optional) Set up and display differential aberrations	**1** Open one or more samples in the View Aberrations window. See Show aberrations for selected samples, on page 32. **2** In the View Aberrations window, click **Aberration**.  The Differential Aberration Setup dialog box appears. **3** Below the diagram for each array, select one of these options. You must assign at least one array to Set 1 and one array to Set 2. • Set 1 – Assigns the array to the first group of arrays. The program compares the aberrations in this group of arrays to the ones you assign to Set 2. • Set 2 – Assigns the array to the second group of arrays. The program compares the aberrations in this group of arrays to the ones you assign to Set 1. • Ignore – The program does not consider the array in the differential aberration analysis. If you have many arrays, it can be easier to use the Define Sets dialog box to assign the arrays to comparison groups. To open this dialog box, click Define Sets. For more information, see the *Reference Guide*. **4** In Select Algorithm, the HyperGeometric algorithm is selected. It is used to evaluate the significance of differences in the detected aberrations between the two comparison groups.	• You must select at least two samples in order to perform differential aberration. • Differential aberration analysis reveals aberrations that are significantly different in different samples. After you assign one or more arrays to each of two groups, the program evaluates the differences in the detected aberrations between the groups.

Table 8 Tasks for creating aberration summaries (continued)

To do this task	Follow these instructions	Comments
	5 Click **Run**. The program evaluates the two sets of arrays, and summarizes the differences in the Graphical Differential Aberration Summary dialog box.	
(Optional) Display probe-based graphical penetrance summary	**1** In the View tab, show the aberrations for selected samples. See Show aberrations for selected samples, above. **2** Under Penetrance, click **Probe**  . The Graphical Penetrance Summary dialog box appears. **3** Mark the box(es) for the chromosomes you want to display in the summary, or click **Select All** to mark all chromosomes. To clear all boxes, click **Deselect All**. **4** To copy the summary to the Clipboard, click **Edit** and then click **Copy Summary to Clipboard**. You can then paste the summary information in the Clipboard into a document of your choice.	• Probe penetrance plots display the percentage of selected arrays that have an aberration at each probe position on the array for the selected chromosomes.

Table 8 Tasks for creating aberration summaries (continued)

To do this task	Follow these instructions	Comments
(Optional) Display graphical intervals summary	**1** In the View tab, show the aberrations for selected samples. See Show aberrations for selected samples, above. **2** Under Penetrance, click **Interval**  . The Graphical Interval Penetrance Summary dialog box appears. **3** To filter the results using an interval filter, **a** Click the arrow next to Filter, and select an interval filter to apply. **b** Click **Apply Filter**. OR To create and apply a new interval filter, **a** Click **Create Filter**. **b** In the Interval Filter dialog box, define the new filter and type a name for it. **c** Click **Apply Filter**.	• Interval penetrance plots display the percentage of selected samples that have an identified aberrant region on the array. You can create and export the plots and tab-delimited tables of the interval penetrance summaries, or copy the summary to the Clipboard and then paste it into another program or document. • For more information on the Graphical Interval Penetrance Summary dialog box, see the *Reference Guide*.

4 Reviewing and Signing Off Results

In Agilent CytoGenomics 1.5, Workflows are used to automate feature extraction and/or analysis of CGH and CGH+SNP data. This chapter gives instructions on how to search for workflow samples and review and sign off the results.

Overview of Data Review

The following diagram gives an overview of review and sign off of analyzed samples. Only users with the role of Scientist or Administrator can sign off samples.

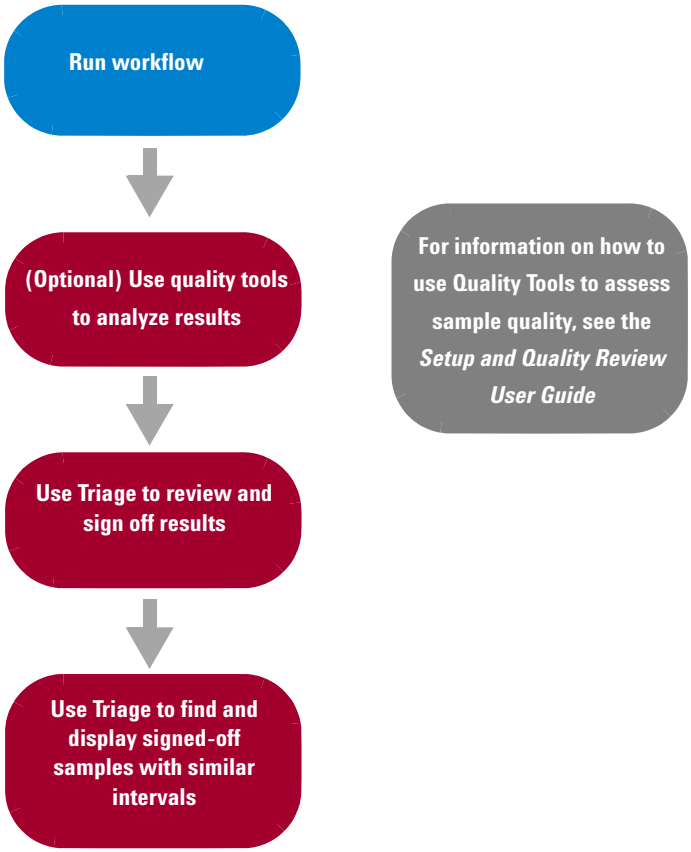

Figure 7 Overview of analyzed sample review and sign off

Using Triage View to Review and Sign Off Results

Once a workflow is completed, you display and check the analysis results in the Triage View. The following diagram shows you what you can do in Triage View.

NOTE Users with the role of Scientist or Administrator can open samples in Triage View and perform all functions. Users with the role of Technician can open Triage View and perform all functions except for Sign Off of results.

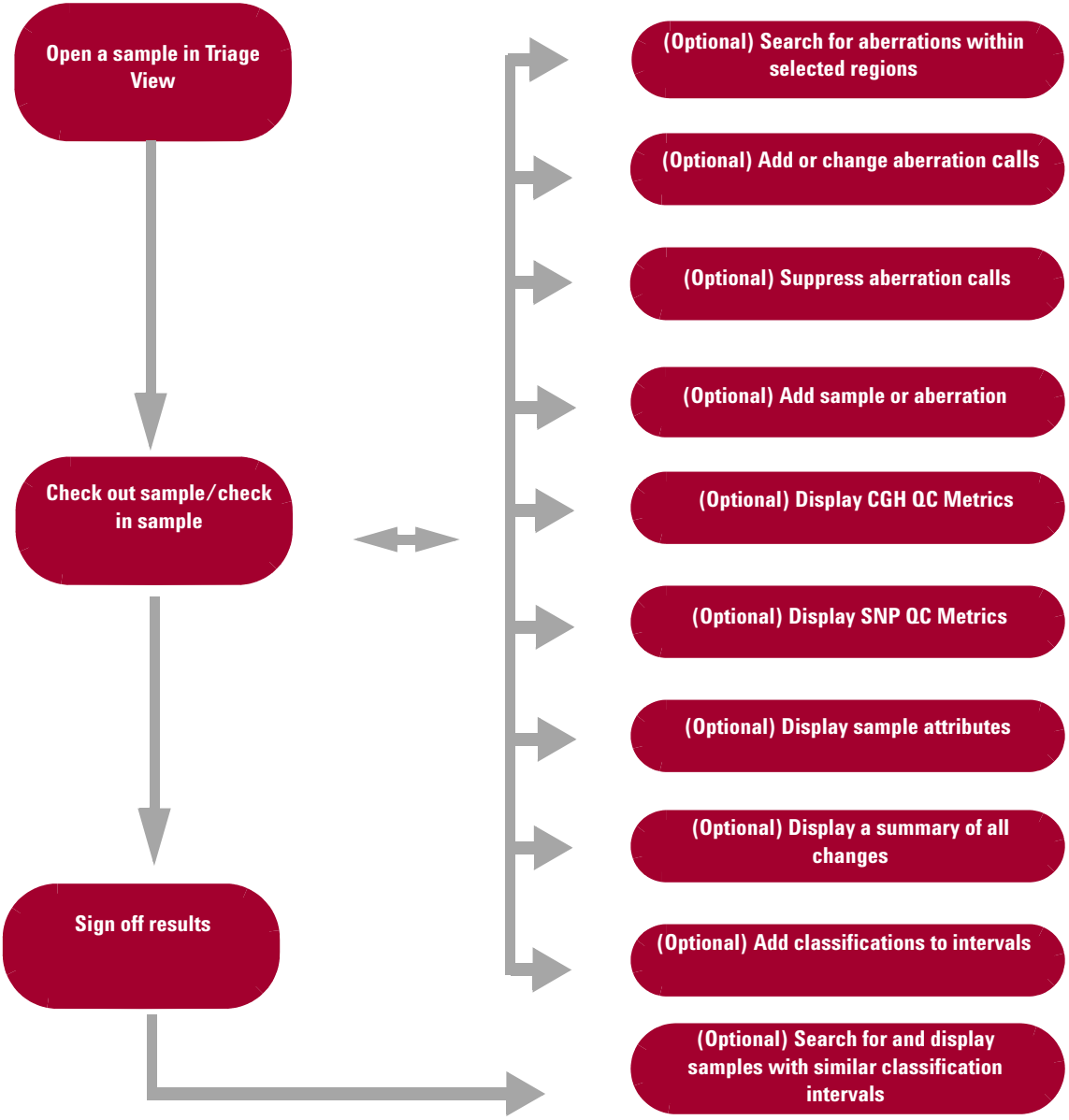

Figure 8 Using Triage View to review and sign off results

How results are displayed

In the Triage View, extracted data and analysis results are tabulated and displayed along with depictions of the genome, selected chromosome, and selected genes of the species whose array data you are analyzing.

There are four main views in the Triage View.

- **Genome View** – A graphical representation of the entire genome for the selected species. Use this view to select the chromosome to show in the other views.
- **Chromosome View** – A graphical representation of the selected chromosome, displayed with cytobands and a plot area. Click or drag the mouse to select a region to display in the Gene View.
- **Gene View** – A more detailed view of the chromosomal region selected in the Chromosome View.
- **Tab View** – Displays CGH design annotation and log ratio data, and CGH+SNP genotype data related to the chromosome you select in Chromosome View. Within this table, you can search for aberrations, and select to suppress or make changes to selected intervals, and create interval notes. In addition, you can add or change calls.

For more information on the Triage View window features and dialog boxes, see the *Reference Guide*.

Tasks for Reviewing and Signing Off Results

The following table contains how-to instructions for using the Triage View to review and sign off analysis results for a sample. For information on the different views within the window, see the *Reference Guide*.

Table 9 Tasks for reviewing and signing off results

To do this	Follow these instructions	Comments
Open a sample in Triage View	**1** In the Analysis tab, click **Monitor**. **2** Next to **Search Type**, select a criterion to use for searching. For example, select **User** to select jobs run by a specific user. **3** Next to **Operator**, select an operator to apply to the search. **4** Next to **Value**, type the value to use for the search. **5** Click **Search**. The jobs that meet the selected criterion are displayed. **6** Locate the job you wish to review. **7** Under Actions, click **Review**. **8** Follow step 3 through step 5 below to open the sample in Triage View. OR **1** In the Analysis tab, click **Review**. The Sample Search table appears. The samples for the most recent workflow job are displayed. **2** Search for a sample. See "Searching for Analyzed Samples" on page 26. **3** Locate the desired sample in the table, and click **Analyzed, Checked Out** (if the sample is currently checked out by you,) **Checked In**, or **Reviewed**. **4** If more than one analysis result is available, in the Analyzed Sample dialog box, under Select, mark to select the name for the sample results you wish to view. **5** Click **OK**. The selected results for the sample appear in the Triage View.	• Samples with a Status of *Analyzed* have analysis results available for display in Triage View. • Samples that are checked out have a Status of *Checked Out*. You can open a sample that is checked out by another user, but you cannot check it out or change it. • Samples that were changed and checked in have a Status of *Checked In*. These samples are available for anyone to check out. • Samples that were signed off have a status of *Reviewed*. You can display the sample results, but you cannot make further changes. • In order to change results, you must first *Check Out* the sample from the Triage View. After you make changes, you must *Check In* the sample in order to save the changes.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Search for aberrations	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** In the Tab View, click **Amp/Del Intervals** or **LOH Intervals** to select the type of data you want to show. **3** In the command ribbon, click **Search**, **a** Select **Contained Within** to find aberrations within the start/stop location. **b** Next to **Chromosome**, click the arrow and select the name of the chromosome to search. For example, select **chr1** for chromosome 1. OR **a** Select **Overlapping** to find aberrations that overlap the specified locations. **b** Next to **Start** and **Stop**, type the start and stop location of the interval. **4** Click **Next** to find the next instance that matches the criteria, or click **Prev** to go to the previous instance that matches the criteria. The cursors in the Chromosome and Gene views move to the location. **5** To clear the criteria search boxes, click **Clear**.	• Samples that are checked out have a Status of *Checked Out*. • You can open a sample that is checked out by another user, but you cannot check it out or change it. • The LOH Intervals tab is only available for CGH+SNP samples that were analyzed using the LOH Algorithm.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Add an aberration call	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** In the Tab View, click **Amp/Del Intervals** or **LOH Intervals** to select the type of data you want to show. **4** In the command ribbon, click **Change Call** and then click **Add Call**. The Add Aberration Call dialog box appears. **5** Type the information for the aberration you want to add. **6** Click the arrow next to Call, and select if the aberration is an Amplification or Deletion. **7** Click **Add**. **8** Click **Check In**.	• Samples that are checked out have a Status of *Checked Out*. You can open a sample that is checked out by another user, but you cannot check it out or change it. • The LOH Intervals tab is only available for CGH+SNP samples that were analyzed using the LOH algorithm. • Click **Reset** to clear the boxes in the dialog box. • Changes made in Triage View are not saved until you click **Check In** or **Sign Off**. Once you click **Sign Off**, the record is locked to further changes.
(Optional) Suppress an aberration call	**1** Open a sample in Triage View.See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** In the **Amp/Del Intervals** or **LOH Intervals** tab, under Suppress, select the box next to each call you want to suppress. If you change your mind, clear the box. **4** When you are finished, click **Check In** to save and check in the changes.	• Changes made in Triage View are not saved until you click **Check In** or **Sign Off**. Once you click **Sign Off**, the record is locked to further changes.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Suppress or clear suppression for all aberration calls	To suppress all aberration calls **1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** In the command ribbon, click **Change Call.** **4** Click **Suppress All**. **5** In the Confirm dialog box, click **Yes**. **6** When you are finished, click **Check In** to save and check in the changes. To clear suppression of all aberration calls. **1** In the command ribbon, click **Change Call.** **2** Click **Unsuppress All**. **3** In the Confirm dialog box, click **Yes**. **4** When you are finished, click **Check In** to save and check in the changes.	• Changes made in Triage View are not saved until you click **Check In** or **Sign Off**. Once you click **Sign Off**, the record is locked to further changes.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Suppress aberration calls for an entire track	To suppress aberration calls for a track **1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** In the command ribbon, click **Change Call.** **4** Click **Auto Suppress**. The Auto Suppress dialog box appears. **5** Next to **Select Track,** click the arrow and select the track that contains the calls you want to suppress. **6** To suppress calls that fall in overlapped intervals, mark **Suppress partly overlapped interval**. **7** Click **Apply**. **8** When you are finished, click **Check In** to save and check in the changes. To clear suppression of calls in a track **1** In the command ribbon, click **Change Call.** **2** Click **Undo Suppress**.	• For information on tracks, see the *Reference Guide*. • Changes made in Triage View are not saved until you click **Check In** or **Sign Off**. Once you click **Sign Off**, the record is locked to further changes.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Change an aberration call	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** In the **Amp/Del Intervals** or **LOH Intervals** tab, in the row for the aberration you want to change, click **Edit**. The Edit Aberration dialog box appears. **4** Type the changes you want to make to aberration call. **5** Click **Apply**. **6** When you are finished editing, click **Cancel** or the red X at the upper right corner of the dialog box to close it. **7** Click **Check In** to save and check in the changes.	• Changes made in Triage View are not saved until you click **Check In** or **Sign Off**. Once you click **Sign Off**, the record is locked to further changes. • Intervals that have been changed show a state of *Edited*.
(Optional) Add notes for an aberration call	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** Click the **Amp/Del Intervals** or **LOH Intervals** tab. **4** In the row for the aberration you want to add a note, click **Notes**. The Notes dialog box appears. **5** Type the text for the note you want to add for the aberration call. **6** Click **Add**. The note appears in the notes table. **7** To include the note in the triage sign-off report, select **Show in report**. **8** When you are finished, click **Check In** to save and check in the changes.	• Changes made in Triage View are not saved until you click **Check In** or **Sign Off**. Once you click **Sign Off**, the record is locked to further changes.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Add sample notes	**1** Open a sample in Triage View.See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** Click **Sample Notes**. The Sample Notes dialog box appears. **4** Type a note you want to add for the sample. **5** Click **Add**. **6** To include the note in the triage sign-off report, select **Show in report**. To add a standardized note to the sample notes **1** Perform steps 1-3, above to open the Sample Notes dialog box. **2** Click **Add Standard Note**. The Add Standard Note dialog box appears. **3** Under Standard Notes, click the note you want to add to the triage sign-off report. **4** Click **Add**. **5** Click **OK** The note appears in the notes table. **6** To include the note in the triage sign-off report, select **Show in report**. To add an interval or SNP Interval note to the sample notes **1** Perform steps 1-3, above to open the Sample Notes dialog box. **2** Click **Interval Notes or SNP Interval Notes**. A list of interval notes for the sample appears. **3** Select **Show in report** for each interval note you want to include in the triage sign-off report. **4** Click **Save.** **5** Click **Close** to close the dialog box.	• Changes made in Triage View are not saved until you click **Check In** or **Sign Off**. Once you click **Sign Off**, the record is locked to further changes.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Display a summary of all changes	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** Click **Audit Trail**. The Audit Trail dialog box appears. **4** When you are finished, click **Close** to close the dialog box.	• The Audit Trail contains all changes that were made to the sample results, along with records of who checked in and out the sample and the dates and times.
(Optional) Display CGH QC Metrics	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** On the command ribbon, click **CGH QC**. The QC Metrics Table appears.	• For more information on the QC Metrics Table, see the *Reference Guide*.
(Optional) Display SNP QC Metrics	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** On the command ribbon, click **SNP QC**. The SNP CN QC Metrics Table appears.	• SNP CN QC Metrics are displayed only for samples that were analyzed with SNP algorithms.
(Optional) Search for gene or genomic location	**1** Open an analyzed sample in Triage View window. See Open a sample in Triage View on page 49. **2** On the command ribbon, click **Go to**. The Go to Gene/Genomic location dialog box appears. **3** Under RefSeq by Symbol, select a gene to search for. OR Under Genomic Location, select a chromosome and then type a base position to search for. **4** Click **Go**. The program finds the gene or genomic location in the Genomic Viewer.	• It can take several seconds or more to display the Go to Gene/Genomic location dialog box. This is because the program searches for all the genes in the sample.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Display sample attributes	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** On the command ribbon, click **Sample Info**. The Attributes dialog box appears that shows attributes and values. **3** Click **Close**.	• Only sample attributes that were marked for display in the Show/Hide Columns dialog box are displayed. See the *Reference Guide* for information on the Show/Hide Columns dialog box. • Sample attributes displayed in Triage View are read-only.
(Optional) Add a classification to an interval	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** In the Tab View, click **Amp/ Del Intervals** or **LOH Intervals**. The table of amplification and deletion intervals or LOH intervals appears. **4** In the row for the interval, under Classification, right-click the mouse and select **Add classification to this interval**. The Add classification dialog box appears. **5** Next to **Select Classification**, click the arrow and select the desired classification. **6** Click **Add**. The selected classification appears in the interval row. **7** Click **Check In** to save the change and close Triage View.	• Classifications that appear in the Add classification list are those that were created in the Config tab. • To add another annotation to the interval, repeat the procedure. • When a classification is configured to show as a column in Triage View, a separate column for that classification appears in the Table View. A number shown in brackets [] next to the name indicates the total number of similar intervals found. Numbers shown in the interval rows indicate the number of matching similar intervals found.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Add a classification to all intervals	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** In the Tab View, click **Amp/ Del Intervals** or **LOH Intervals**. The table of amplification and deletion intervals or LOH intervals appears. **4** In the row for the interval, under Classification, right-click the mouse and select **Add classification to all unclassified intervals**. The Add classification dialog box appears. **5** Next to **Select Classification**, click the arrow and select the desired classification. **6** Click **Add**. The selected classification appears in the interval rows for previously unclassified intervals. **7** Click **Check In** to save the change and close Triage View.	• Classifications that appear in the Add classification list are those that were created in the Config tab. • To add another classification to the intervals, repeat the procedure.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Remove annotation from one or all intervals	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Check Out** to check out the sample. **3** In the Tab View, click **Amp/ Del Intervals** or **LOH Intervals**. The table of amplification and deletion intervals or LOH intervals appears. To remove an annotation from one interval **a** In the row for the interval, under Annotation, right-click the mouse and select **Remove annotation from this interval**. **b** The Remove annotation dialog box appears. **c** Next to **Select Annotation**, click the arrow and select the desired annotation. **d** Click **Remove**. **e** The selected annotation is removed from the selected interval. **f** Click **Check In** to save the change and close Triage View. To remove an annotation from all intervals **a** In the row for the interval, under Annotation, right-click the mouse and select **Remove annotation from all intervals**. **b** The Remove annotation dialog box appears. **c** Next to **Select Annotation**, click the arrow and select the desired annotation. **d** Click **Remove**. **e** The selected annotation is removed from all intervals. **f** Click **Check In** to save the changes and close Triage View.	• Classifications that appear in the Remove classification list are those that were created in the Config tab.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
Sign off results	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Click **Sign Off**. The Confirm dialog box appears. **3** Click **OK** to sign off the results.	• Once the results are signed off, the results are permanently locked, and cannot be changed. • Only users with the role of Scientist or Administrator can sign off results.
(Optional) Search for samples containing similar intervals	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** In the Tab View, click **Amp/Del Intervals or LOH Intervals**. **3** Locate the interval you want to use to search for similar intervals. **4** Under **Classification**, right-click and select **Search similar interval**. **5** Click **Select Classification** and select a classification to use for the search OR Click **Select Query** and select a saved query to use for the search. The program searches for reviewed samples that have one or more similar intervals and displays them in the Gene View.	• Only samples that were signed off are searched for similar intervals. (Samples that are signed off have a status of *Reviewed*.) • To open a sample that was found in the search, double-click in the Query Result pane for that sample.
(Optional) Change the search threshold for interval search	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** In the Tab View, click **Amp/Del Intervals or LOH Intervals**. **3** Locate the interval you want to use to search for similar intervals. **4** Under **Classification**, right-click and select **Change search threshold**. The Change search threshold dialog box appears. **5** Next to threshold, type a value to be used for the search threshold. **6** Click **Ok**.	• The default threshold is .70. A higher number makes the search more stringent. A lower number makes the search more likely to find similar intervals.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Search for gene information	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** In the Tab View, click **Amp/Del Intervals or LOH Intervals**. **3** For the interval of interest, right-click Gene Name and select a database to search for the gene information. The View Gene or OMIM (if you selected OMIM) dialog box appears. **4** Next to the gene of interest, click **Search** to open the selected database and locate information for the gene. (For OMIM, click the OMIM Id.) The selected database opens in your browser and displays the information for the selected gene.	• If a gene name appears in black or white, it does not have an OMIM Id associated with it, and OMIM does not appear as a database selection. • If a gene name appears in red or blue, it does have an OMIM Id associated with it, and OMIM appears as a database selection. Genes displayed in red are of morbid type.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Create a custom track	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Right- click anywhere within the log ratio plot area in Gene View, then click **Create Track**. The Create Track dialog box appears. See "Create Track" on page 304. **3** In the dialog box, set the Name, Description and Color. **4** In the dialog box, **a** Select **User Defined**. **b** Under **Chromosome**, select the chromosome for the track. **c** Under **Start** and **Stop**, type the start and stop of the region for the new track. **d** Under **Select Track Source**, click **Aberration Results**. OR, to generate a track for the entire gene **a** Select **For complete gene view**. **b** Under **Select Track Source**, click **Aberration Results**. OR, to generate a track for current the region defined by the cursor **a** Select **For aberrant region below cursor**. **b** Under **Chromosome**, select the chromosome for the track. **c** Under **Start** and **Stop**, type the start and stop of the region for the new track. **d** Under **Select Track Source**, click **Aberration Results**. **5** Click **OK**.	• When you create a track, you create a list of the genes in a contiguous chromosomal region that you select. • You can turn on and off the display of tracks in the Gene View and in Reports from the Track Settings dialog box. See the *Reference Guide* for information on the Track Settings dialog box. • You can also create a custom track from a query in Config > Tracks > Create Track From Query. For more information, see the *Setup and Quality Review User Guide*.

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Create a signal intensity bar chart	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Right- click anywhere within the log ratio plot area in Gene View, then click **Show Intensity Bar Charts**. The Create Signal Bar Chart dialog box appears. **3** Under Set Chromosome Start-Stop, select the region to use for creating the bar chart. Choices include a user-defined region, the complete gene view, or for the current region selected by the cursor. **4** Click **OK**. A Median Signal Intensity bar chart is created showing red and green signal intensities for all selected microarrays.	• A signal bar chart is a histogram that displays the median signal intensities in a genomic region of selected Agilent arrays. • For more information on the Create Signal Bar Chart dialog box, see the *Reference Guide*.
(Optional) Display track in UCSC browser	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Right-click Gene View, and click **Show in UCSC**. The View coordinates in UCSC browser dialog box appears. **3** Complete the dialog box with the track parameters, and click **OK**. The UCSC Browser appears, if you are connected to the Internet. You may need to enable pop-ups or set other preferences on the UCSC Web site; see the browser help for information.	• For more information on the Triage View window, see the *Reference Guide.*

Table 9 Tasks for reviewing and signing off results (continued)

To do this	Follow these instructions	Comments
(Optional) Change how tracks are displayed	**1** Open a sample in Triage View. See Open a sample in Triage View on page 49. **2** Right-click anywhere within the log ratio plot area in Gene View, and click **Track Settings**. The Track Settings dialog box appears. **3** Select tracks and how to display them. **4** Click **OK**.	• For more information on the Track Settings dialog box, see the *Reference Guide*.

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In this book

This guide describes how to use the Agilent CytoGenomics 1.5 software to run workflows and display reports and aberrations. The functions described in this guide are typically performed by users with an assigned role of "Technician." However, tasks described in this guide are available to users with an assigned role of "Technician," "Scientist," or "Administrator."

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